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SEQUENCE LISTING

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<120> Method for Studying Protein Interactions in Vivo

<130> 11785-3PCT

<140> filed herewith

<141> 1999-09-02

<150> 60/135,835

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<150> 60/099,068

<151> 1998-09-03

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 918

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)..(719)

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tg tgc ccc cac agg ctg ctg cca ccg ctg ctg ctg cta gct ctg 47

Cys Pro His Arg Leu Leu Pro Pro Leu Leu Leu Leu Leu Ala Leu

1

5

10

15

ctg ctc gct gcc agc cca gga ggc gcc ttg gcg cgg tgc cca ggc tgc 95

Leu Leu Ala Ala Ser Pro Gly Gly Ala Leu Ala Arg Cys Pro Gly Cys

20

25

30

ggg caa ggg gtg cag gcg ggt tgt cca ggg ggc tgc gtg gag gag gag 143

Gly Gln Gly Val Gln Ala Gly Cys Pro Gly Gly Cys Val Glu Glu Glu

35

40

45

gat ggg ggg tcg cca gcc gag ggc tgc gcg gaa gct gag ggc tgt ctc 191

Asp Gly Gly Ser Pro Ala Glu Gly Cys Ala Glu Ala Glu Gly Cys Leu

50	55	60	
agg agg gag ggg cag gag tgc ggg gtc tac acc cct aac tgc gcc cca			239
Arg Arg Glu Gly Gln Glu Cys Gly Val Tyr Thr Pro Asn Cys Ala Pro			
65	70	75	
gga ctg cag tgc cat ccg ccc aag gac gac gag gcg cct ttg cgg gcg			287
Gly Leu Gln Cys His Pro Pro Lys Asp Asp Glu Ala Pro Leu Arg Ala			
80	85	90	95
ctg ctg ctc ggc cga ggc cgc tgc ctt ccg gcc cgc gcg cct gct gtt			335
Leu Leu Leu Gly Arg Gly Arg Cys Leu Pro Ala Arg Ala Pro Ala Val			
	100	105	110
gca gag gag aat cct aag gag agt aaa ccc caa gca ggc act gcc cgc			383
Ala Glu Glu Asn Pro Lys Glu Ser Lys Pro Gln Ala Gly Thr Ala Arg			
	115	120	125
cca cag gat gtg aac cgc aga gac caa cag agg aat cca ggc acc tct			431
Pro Gln Asp Val Asn Arg Arg Asp Gln Gln Arg Asn Pro Gly Thr Ser			
	130	135	140
acc acg ccc tcc cag ccc aat tct gcg ggt gtc caa gac act gag atg			479
Thr Thr Pro Ser Gln Pro Asn Ser Ala Gly Val Gln Asp Thr Glu Met			
	145	150	155
ggc cca tgc cgt aga cat ctg gac tca gtg ctg cag caa ctc cag act			527
Gly Pro Cys Arg Arg His Leu Asp Ser Val Leu Gln Gln Leu Gln Thr			
160	165	170	175
gag gtc tac cga ggg gct caa aca ctc tac gtg ccc aat tgt gac cat			575
Glu Val Tyr Arg Gly Ala Gln Thr Leu Tyr Val Pro Asn Cys Asp His			
	180	185	190
cga ggc ttc tac cgg aag cgg cag tgc cgc tcc tcc cag ggg cag cgc			623
Arg Gly Phe Tyr Arg Lys Arg Gln Cys Arg Ser Ser Gln Gly Gln Arg			
	195	200	205
cga ggt ccc tgc tgg tgt gtg gat cgg atg ggc aag tcc ctg cca ggg			671
Arg Gly Pro Cys Trp Cys Val Asp Arg Met Gly Lys Ser Leu Pro Gly			
	210	215	220
tct cca gat ggc aat gga agc tcc tcc tgc ccc act ggg agt agc ggc			719
Ser Pro Asp Gly Asn Gly Ser Ser Ser Cys Pro Thr Gly Ser Ser Gly			
	225	230	235
taaagctggg ggatagaggg gctgcagggc cactggaagg aacatggagc tgtcatcact			779

caacaaaaaa ccgaggccct caatccacct tcaggccccg ccccatgggc ccctcaccgc 839

tgggttgaaa gagtggttgggt gttggctggg gtgtcaataa agctgtgctt ggggtcgctg 899

aaaaaaaaaa aaaaaaaaaa 918

<210> 2

<211> 239

<212> PRT

<213> Homo sapiens

<400> 2

Cys Pro His Arg Leu Leu Pro Pro Leu Leu Leu Leu Leu Ala Leu Leu
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Leu Ala Ala Ser Pro Gly Gly Ala Leu Ala Arg Cys Pro Gly Cys Gly
20 25 30

Gln Gly Val Gln Ala Gly Cys Pro Gly Gly Cys Val Glu Glu Glu Asp
35 40 45

Gly Gly Ser Pro Ala Glu Gly Cys Ala Glu Ala Glu Gly Cys Leu Arg
50 55 60

Arg Glu Gly Gln Glu Cys Gly Val Tyr Thr Pro Asn Cys Ala Pro Gly
65 70 75 80

Leu Gln Cys His Pro Pro Lys Asp Asp Glu Ala Pro Leu Arg Ala Leu
85 90 95

Leu Leu Gly Arg Gly Arg Cys Leu Pro Ala Arg Ala Pro Ala Val Ala
100 105 110

Glu Glu Asn Pro Lys Glu Ser Lys Pro Gln Ala Gly Thr Ala Arg Pro
115 120 125

Gln Asp Val Asn Arg Arg Asp Gln Gln Arg Asn Pro Gly Thr Ser Thr
130 135 140

Thr Pro Ser Gln Pro Asn Ser Ala Gly Val Gln Asp Thr Glu Met Gly
145 150 155 160

Pro Cys Arg Arg His Leu Asp Ser Val Leu Gln Gln Leu Gln Thr Glu
165 170 175

Val Tyr Arg Gly Ala Gln Thr Leu Tyr Val Pro Asn Cys Asp His Arg
180 185 190

Gly Phe Tyr Arg Lys Arg Gln Cys Arg Ser Ser Gln Gly Gln Arg Arg
 195 200 205

Gly Pro Cys Trp Cys Val Asp Arg Met Gly Lys Ser Leu Pro Gly Ser
 210 215 220

Pro Asp Gly Asn Gly Ser Ser Ser Cys Pro Thr Gly Ser Ser Gly
 225 230 235

<210> 3

<211> 1196

<212> DNA

<213> Renilla reniformis

<220>

<221> CDS

<222> (10)..(945)

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 1 5 10

ata act ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt 99
 Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu
 15 20 25 30

gat tca ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct 147
 Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala
 35 40 45

gtt att ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat 195
 Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His
 50 55 60

gtt gtg cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt 243
 Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu
 65 70 75

att ggt atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta 291
 Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu
 80 85 90

ctt gat cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta 339
 Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu
 95 100 105 110

cca aag aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca	387
Pro Lys Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala	
115 120 125	
ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac	435
Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His	
130 135 140	
gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat	483
Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp	
145 150 155	
att gaa gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg	531
Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met	
160 165 170	
gtt ttg gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc	579
Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile	
175 180 185 190	
atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc	627
Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe	
195 200 205	
aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa	675
Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu	
210 215 220	
atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg	723
Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg	
225 230 235	
aat tat aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt	771
Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe	
240 245 250	
att gaa tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc	819
Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala	
255 260 265 270	
aag aag ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt	867
Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe	
275 280 285	
tcg caa gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc	915
Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe	
290 295 300	

gtt gag cga gtt ctc aaa aat gaa caa taa ttactttggt tttttattta 965
 Val Glu Arg Val Leu Lys Asn Glu Gln
 305 310

cattttttccc gggtttaata atataaatgt catttttcaac aattttattt taactgaata 1025
 tttcacaggg aacattcata tatgttgatt aatttagctc gaactttact ctgtcatatc 1085
 attttggaat attacctctt tcaatgaaac tttataaaca gtggttcaat taattaatat 1145
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<210> 4

<211> 311

<212> PRT

<213> Renilla reniformis

<400> 4

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 20 25 30

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
 35 40 45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
 50 55 60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65 70 75 80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
 85 90 95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
 100 105 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
 115 120 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
 130 135 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu

145		150		155		160
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu						
	165		170		175	
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg						
	180		185		190	
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu						
	195		200		205	
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro						
	210		215		220	
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr						
	225		230		235	240
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu						
	245		250		255	
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys						
	260		265		270	
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln						
	275		280		285	
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu						
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Arg Val Leu Lys Asn Glu Gln						
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<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(543)

<400> 5

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1 5 10 15	

gcc ttc gcc tcg tgc tgc att gct gct tac cgc ccc agt gag acc ctg	96
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Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu	
20 25 30	
tgc ggc ggg gag ctg gtg gac acc ctc cag ttc gtc tgt ggg gac cgc	144
Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg	
35 40 45	
ggc ttc tac ttc agc agg ccc gca agc cgt gtg agc cgt cgc agc cgt	192
Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg	
50 55 60	
ggc atc gtt gag gag tgc tgt ttc cgc agc tgt gac ctg gcc ctc ctg	240
Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu	
65 70 75 80	
gag acg tac tgt gct acc ccc gcc aag tcc gag agg gac gtg tcg acc	288
Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr	
85 90 95	
cct ccg acc gtg ctt ccg gac aac ttc ccc aga tac ccc gtg ggc aag	336
Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys	
100 105 110	
ttc ttc caa tat gac acc tgg aag cag tcc acc cag cgc ctg cgc agg	384
Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg	
115 120 125	
ggc ctg cct gcc ctc ctg cgt gcc cgc cgg ggt cac gtg ctc gcc aag	432
Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys	
130 135 140	
gag ctc gag gcg ttc agg gag gcc aaa cgt cac cgt ccc ctg att gct	480
Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala	
145 150 155 160	
cta ccc acc caa gac ccc gcc cac ggg ggc gcc ccc cca gag atg gcc	528
Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala	
165 170 175	
agc aat cgg aag tga	543
Ser Asn Arg Lys	
180	

<210> 6

<211> 180

<212> PRT

<213> Homo sapiens

<400> 6

Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu Thr Phe Leu
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Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu
 20 25 30

Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
 35 40 45

Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
 50 55 60

Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
 65 70 75 80

Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
 85 90 95

Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
 100 105 110

Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
 115 120 125

Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
 130 135 140

Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
 145 150 155 160

Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
 165 170 175

Ser Asn Arg Lys
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<210> 7

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(717)

<220>

<223> Description of Artificial Sequence: humanized
green fluorescent protein cDNA

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 gaa ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
 ggg gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
 acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
 tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	
 cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
 acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
 aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
 gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
 tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
 atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	

cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct 576
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct 624
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg 672
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga 717
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 8

<211> 238

<212> PRT

<213> Artificial Sequence

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 9

<211> 333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(333)

<400> 9

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 1 5 10 15

tgg gga cct gac cca gcc gca gcc ttt gtg aac caa cac ctg tgc ggc 96
 Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30

tca cac ctg gtg gaa gct ctc tac cta gtg tgc ggg gaa cga ggc ttc 144
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45

ttc tac aca ccc aag acc cgc cgg gag gca gag gac ctg cag gtg ggc 192
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60

cag gtg gag ctg ggc ggg ggc cct ggt gca ggc agc ctg cag ccc ttg 240
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80

gcc ctg gag ggg tcc ctg cag aag cgt ggc att gtg gaa caa tgc tgt 288
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95

acc agc atc tgc tcc ctc tac cag ctg gag aac tac tgc aac tag 333
 Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
 100 105 110

<210> 10

<211> 110

<212> PRT

<213> Homo sapiens

<400> 10

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
 1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
 20 25 30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
 35 40 45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
 50 55 60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
 65 70 75 80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
 85 90 95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
 100 105 110